

SEQUENCE LISTING

<110> SIMMONS, ANTHONY
CHEN, JIANMIN

<120> COMPOSITIONS AND METHODS FOR HERPES SIMPLEX PROPHYLAXIS
AND TREATMENT

<130> UTEG:263WO

<140> UNKNOWN
<141> 2004-07-26

<150> 60/489,984
<151> 2003-07-23

<160> 36

<170> PatentIn Ver. 2.1

<210> 1
<211> 921
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 1

atggagacag acacactcct gctatggta ctgctgctct gggttccagg ttccactgg 60
gacgcggccc agccggccag ggcgcgcgc cgtacgaagc ttggtaccga gctcgatcc 120
gacatccaga tgaccaggc tccatcctcc ttatctgcct ctctgggaga aagagtcagt 180
ctcaactgtc gggcaagtca ggaaattagt gcttacttaa gctggctca gcagaaacca 240
gatggaacta ttaaacgcct gatctacgccc gcatttactt tagattctgg tggccaaaa 300
aggttcagtg gcagtaggtc tgggtcagat tattctctca ccatcagcag ccttggatct 360
gaagattttt cagacttata ctgtctacaa tatgtctttt atccgctcac gttcggtgct 420
gggaccaagg tggagctggg cgggtggcgg tcgggtggag gaggcagcgg aggcgggtgg 480
tcggtaaggc tgcaggagtc tggacctgag ctggtaagc ctggggcttc agtgaagatg 540
tcctgcaagg cttctggcta cacattcaca agcttctatg tacactgggt gaagcagagg 600
cctggacagg gacttggatg gattggatgg attttatcctg gacatagtag tactaagtac 660
aatgagaagt tcatggccaa gaccatattt actgcggaca aatcctccag cacagcctac 720
attttgctca gcagcctgac ctctgaggac tctgcgatatttctgtac aaggcaggag 780
gtacgactct ggtacttcga tgcgtgggc gcagggacca cggtcaccgt ctccgcggcc 840
gctcgaggag ggccccaaaca aaaactcatc tcagaagagg atctgaatag cggccgtcgac 900
catcatcatc atcatcattt a 921

<210> 2

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 2

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr
20 25 30

Lys Leu Gly Thr Glu Leu Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
35 40 45

Ser Ser Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg
50 55 60

Ala Ser Gln Glu Ile Ser Ala Tyr Leu Ser Trp Leu Gln Gln Lys Pro
65 70 75 80

Asp Gly Thr Ile Lys Arg Leu Ile Tyr Ala Ala Ser Thr Leu Asp Ser
85 90 95

Gly Val Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser
100 105 110

Leu Thr Ile Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys
115 120 125

Leu Gln Tyr Ala Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
130 135 140

Glu Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
165 170 175

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
180 185 190

Tyr Val His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
195 200 205

Gly Trp Ile Tyr Pro Gly His Ser Ser Thr Lys Tyr Asn Glu Lys Phe
210 215 220

Met Gly Lys Thr Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
225 230 235 240

Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
245 250 255

Thr Arg Gln Glu Val Arg Leu Trp Tyr Phe Asp Val Trp Gly Ala Gly
260 265 270

Thr Thr Val Thr Val Ser Ala Ala Ala Arg Gly Gly Pro Glu Gln Lys
275 280 285

Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
290 295 300

His His
305

<210> 3
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Primer

<400> 3
tggtgaaaatggatacag 20

<210> 4
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 4
ggtgatatcg tgatracmca rgatgaactc tc 32

<210> 5
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 5
ggtgatatcw tgmtgaccca awctccactc tc 32

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 6
ggtgatatcg tkctcacyca rtctccagca at 32

<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 7
ctgwtgttctt ggattcctg 19

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 8
gtgctctgga ttcgggaa

18

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 9
tcagcttcyt gctaattcgt g

21

<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 10
tgggttatctg gtrcstgtg

19

<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11
gttcmaggt rccagatgt

19

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12
tgttttcaag gtrccagatg t

21

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13
ctstggttgt ctgggtttga

20

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14
tgctkckctg ggttccag

18

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 15
taacccttga ccaggcatcc

20

<210> 16
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 16
gaggtgaagc tgcaggagtc aggacctagc ctggtg

36

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 17
aggtvmaact gcagvagtcw gg

22

<210> 18
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 18
aggvvagct gcagvagtcw gg 22

<210> 19
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 19
actgcaggtr tccactcc 18

<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 20
rctacaggtg tccactcc 18

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 21
gcyclacagmtg tccactcc 18

<210> 22
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 22
actgcaggtr tcctctct 18

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 23
rctrcaggyg tccactct

18

<210> 24
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 24
ccaagctgtg tcctrcc

18

<210> 25
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 25
ccaagctgtg tcctrcc

18

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 26
tggacagacy cvttccckgg

20

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 27
tayttaaaaa rgtgtcmagt gt

22

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 28
ctyttaaaag gkgtccagwg

20

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 29
cytttamatg gtagtccagtg t

21

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 30
atggcagcwg cycaaag

17

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 31
cttttaaaag wtgtccagkg t

21

<210> 32
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 32
 cttcctgatg gcagtggtt 19

<210> 33
 <211> 904
 <212> PRT
 <213> human herpesvirus 1

<400> 33
 Met Arg Gln Gly Ala Pro Ala Arg Gly Arg Arg Trp Phe Val Val Trp
 1 5 10 15

Ala Leu Leu Gly Leu Thr Leu Gly Val Leu Val Ala Ser Ala Ala Pro
 20 25 30

Ser Ser Pro Gly Thr Pro Gly Val Ala Ala Ala Thr Gln Ala Ala Asn
 35 40 45

Gly Gly Pro Ala Thr Pro Ala Pro Pro Ala Pro Gly Ala Pro Pro Thr
 50 55 60

Gly Asp Pro Lys Pro Lys Lys Asn Arg Lys Pro Lys Pro Pro Lys Pro
 65 70 75 80

Pro Arg Pro Ala Gly Asp Asn Ala Thr Val Ala Ala Gly His Ala Thr
 85 90 95

Leu Arg Glu His Leu Arg Asp Ile Lys Ala Glu Asn Thr Asp Ala Asn
 100 105 110

Phe Tyr Val Cys Pro Pro Pro Thr Gly Ala Thr Val Val Gln Phe Glu
 115 120 125

Gln Pro Arg Arg Cys Pro Thr Arg Pro Glu Gly Gln Asn Tyr Thr Glu
 130 135 140

Gly Ile Ala Val Val Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys
 145 150 155 160

Ala Thr Met Tyr Tyr Lys Asp Val Thr Val Ser Gln Val Trp Phe Gly
 165 170 175

His Arg Tyr Ser Gln Phe Met Gly Ile Phe Glu Asp Arg Ala Pro Val
 180 185 190

Pro Phe Glu Glu Val Ile Asp Lys Ile Asn Ala Lys Gly Val Cys Arg
 195 200 205

Ser Thr Ala Lys Tyr Val Arg Asn Asn Leu Glu Thr Thr Ala Phe His
 210 215 220

Arg Asp Asp His Glu Thr Asp Met Glu Leu Lys Pro Ala Asn Ala Ala
 225 230 235 240

Thr Arg Thr Ser Arg Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro
 245 250 255

Ser Arg Val Glu Ala Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile
 260 265 270

Val Glu Glu Val Asp Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val
 275 280 285

Leu Ala Thr Gly Asp Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg
 290 295 300
 Glu Gly Ser His Thr Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys
 305 310 315 320
 Gln Val Asp Gly Phe Tyr Ala Arg Asp Leu Thr Thr Lys Ala Arg Ala
 325 330 335
 Thr Ala Pro Thr Thr Arg Asn Leu Leu Thr Thr Pro Lys Phe Thr Val
 340 345 350
 Ala Trp Asp Trp Val Pro Lys Arg Pro Ser Val Cys Thr Met Thr Lys
 355 360 365
 Trp Gln Glu Val Asp Glu Met Leu Arg Ser Glu Tyr Gly Ser Phe
 370 375 380
 Arg Phe Ser Ser Asp Ala Ile Ser Thr Thr Phe Thr Thr Asn Leu Thr
 385 390 395 400
 Glu Tyr Pro Leu Ser Arg Val Asp Leu Gly Asp Cys Ile Gly Lys Asp
 405 410 415
 Ala Arg Asp Ala Met Asp Arg Ile Phe Ala Arg Arg Tyr Asn Ala Thr
 420 425 430 ..
 His Ile Lys Val Gly Gln Pro Gln Tyr Tyr Leu Ala Asn Gly Gly Phe
 435 440 445
 Leu Ile Ala Tyr Gln Pro Leu Leu Ser Asn Thr Leu Ala Glu Leu Tyr
 450 455 460
 Val Arg Glu His Leu Arg Glu Gln Ser Arg Lys Pro Pro Asn Pro Thr
 465 470 475 480
 Pro Pro Pro Gly Ala Ser Ala Asn Ala Ser Val Glu Arg Ile Lys
 485 490 495
 Thr Thr Ser Ser Ile Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asn His
 500 505 510
 Ile Gln Arg His Val Asn Asp Met Leu Gly Arg Val Ala Ile Ala Trp
 515 520 525
 Cys Glu Leu Gln Asn His Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys
 530 535 540
 Leu Asn Pro Asn Ala Ile Ala Ser Ala Thr Val Gly Arg Arg Val Ser
 545 550 555 560
 Ala Arg Met Leu Gly Asp Val Met Ala Val Ser Thr Cys Val Pro Val
 565 570 575
 Ala Ala Asp Asn Val Ile Val Gln Asn Ser Met Arg Ile Ser Ser Arg
 580 585 590
 Pro Gly Ala Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp
 595 600 605
 Gln Gly Pro Leu Val Glu Gly Gln Leu Gly Glu Asn Asn Glu Leu Arg
 610 615 620

Leu Thr Arg Asp Ala Ile Glu Pro Cys Thr Val Gly His Arg Arg Tyr
 625 630 635 640
 Phe Thr Phe Gly Gly Tyr Val Tyr Phe Glu Glu Tyr Ala Tyr Ser
 645 650 655
 His Gln Leu Ser Arg Ala Asp Ile Thr Thr Val Ser Thr Phe Ile Asp
 660 665 670
 Leu Asn Ile Thr Met Leu Glu Asp His Glu Phe Val Pro Leu Glu Val
 675 680 685
 Tyr Thr Arg His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu
 690 695 700
 Val Gln Arg Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp
 705 710 715 720
 Thr Val Ile His Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Gly
 725 730 735
 Ala Phe Phe Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val
 740 745 750
 Val Met Gly Ile Val Gly Val Val Ser Ala Val Ser Gly Val Ser
 755 760 765 ..
 Ser Phe Met Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val
 770 775 780
 Leu Ala Gly Leu Ala Ala Ala Phe Phe Ala Phe Arg Tyr Val Met Arg
 785 790 795 800
 Leu Gln Ser Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu
 805 810 815
 Leu Lys Asn Pro Thr Asn Pro Asp Ala Ser Gly Glu Gly Glu Gly
 820 825 830
 Gly Asp Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg
 835 840 845
 Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Lys
 850 855 860
 Lys Lys Gly Thr Ser Ala Leu Leu Ser Ala Lys Val Thr Asp Met Val
 865 870 875 880
 Met Arg Lys Arg Arg Asn Thr Asn Tyr Thr Gln Val Pro Asn Lys Asp
 885 890 895
 Gly Asp Ala Asp Glu Asp Asp Leu
 900

<210> 34
 <211> 904
 <212> PRT
 <213> human herpesvirus 2

<400> 34
 Met Arg Gly Gly Leu Ile Cys Ala Leu Val Val Gly Ala Leu Val

1	5	10	15
Ala Ala Val Ala Ser Ala Ala Pro Ala Ala Pro Ala Ala Pro Arg Ala			
20	25	30	
Ser Gly Gly Val Ala Ala Thr Val Ala Ala Asn Gly Gly Pro Ala Ser			
35	40	45	
Arg Pro Pro Pro Val Pro Ser Pro Ala Thr Thr Lys Ala Arg Lys Arg			
50	55	60	
Lys Thr Lys Lys Pro Pro Lys Arg Pro Glu Ala Thr Pro Pro Pro Asp			
65	70	75	80
Ala Asn Ala Thr Val Ala Ala Gly His Ala Thr Leu Arg Ala His Leu			
85	90	95	
Arg Glu Ile Lys Val Glu Asn Ala Asp Ala Gln Phe Tyr Val Cys Pro			
100	105	110	
Pro Pro Thr Gly Ala Thr Val Val Gln Phe Glu Gln Pro Arg Arg Cys			
115	120	125	
Pro Thr Arg Pro Glu Gly Gln Asn Tyr Thr Glu Gly Ile Ala Val Val			
130	135	140	
Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Thr Met Tyr Tyr			
145	150	155	160
Lys Asp Val Thr Val Ser Gln Val Trp Phe Gly His Arg Tyr Ser Gln			
165	170	175	
Phe Met Gly Ile Phe Glu Asp Arg Ala Pro Val Pro Phe Glu Glu Val			
180	185	190	
Ile Asp Lys Ile Asn Thr Lys Gly Val Cys Arg Ser Thr Ala Lys Tyr			
195	200	205	
Val Arg Asn Asn Met Glu Thr Thr Ala Phe His Arg Asp Asp His Glu			
210	215	220	
Thr Asp Met Glu Leu Lys Pro Ala Lys Val Ala Thr Arg Thr Ser Arg			
225	230	235	240
Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro Ser Arg Val Glu Ala			
245	250	255	
Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile Val Glu Glu Val Asp			
260	265	270	
Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val Leu Ala Thr Gly Asp			
275	280	285	
Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg Glu Gly Ser His Thr			
290	295	300	
Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys Gln Val Asp Gly Phe			
305	310	315	320
Tyr Ala Arg Asp Leu Thr Thr Lys Ala Arg Ala Thr Ser Pro Thr Thr			
325	330	335	
Arg Asn Leu Leu Thr Thr Pro Lys Phe Thr Val Ala Trp Asp Trp Val			

340

345

350

Pro Lys Arg Pro Ala Val Cys Thr Met Thr Lys Trp Gln Glu Val Asp
 355 360 365

Glu Met Leu Arg Ala Glu Tyr Gly Gly Ser Phe Arg Phe Ser Ser Asp
 370 375 380

Ala Ile Ser Thr Thr Phe Thr Thr Asn Leu Thr Glu Tyr Ser Leu Ser
 385 390 395 400

Arg Val Asp Leu Gly Asp Cys Ile Gly Arg Asp Ala Arg Glu Ala Ile
 405 410 415

Asp Arg Met Phe Ala Arg Lys Tyr Asn Ala Thr His Ile Lys Val Gly
 420 425 430

Gln Pro Gln Tyr Tyr Leu Ala Thr Gly Gly Phe Leu Ile Ala Tyr Gln
 435 440 445

Pro Leu Leu Ser Asn Thr Leu Ala Glu Leu Tyr Val Arg Glu Tyr Met
 450 455 460

Arg Glu Gln Asp Arg Lys Pro Arg Asn Ala Thr Pro Ala Pro Leu Arg
 465 470 475 480

Glu Ala Pro Ser Ala Asn Ala Ser Val Glu Arg Ile Lys Thr Thr Ser
 485 490 495

Ser Ile Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asn His Ile Gln Arg
 500 505 510

His Val Asn Asp Met Leu Gly Arg Ile Ala Val Ala Trp Cys Glu Leu
 515 520 525

Gln Asn His Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys Leu Asn Pro
 530 535 540

Asn Ala Ile Ala Ser Ala Thr Val Gly Arg Arg Val Ser Ala Arg Met
 545 550 555 560

Leu Gly Asp Val Met Ala Val Ser Thr Cys Val Pro Val Ala Pro Asp
 565 570 575

Asn Val Ile Val Gln Asn Ser Met Arg Val Ser Ser Arg Pro Gly Thr
 580 585 590

Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp Gln Gly Pro
 595 600 605

Leu Ile Glu Gly Gln Leu Gly Glu Asn Asn Glu Leu Arg Leu Thr Arg
 610 615 620

Asp Ala Leu Glu Pro Cys Thr Val Gly His Arg Arg Tyr Phe Ile Phe
 625 630 635 640

Gly Gly Gly Tyr Val Tyr Phe Glu Glu Tyr Ala Tyr Ser His Gln Leu
 645 650 655

Ser Arg Ala Asp Val Thr Thr Val Ser Thr Phe Ile Asp Leu Asn Ile
 660 665 670

Thr Met Leu Glu Asp His Glu Phe Val Pro Leu Glu Val Tyr Thr Arg

675	680	685
His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu Val Gln Arg		
690	695	700
Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp Thr Val Ile		
705	710	720
Arg Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Cys Ala Phe Phe		
725	730	735
Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val Val Met Gly		
740	745	750
Val Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser Ser Phe Met		
755	760	765
Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val Leu Ala Gly		
770	775	780
Leu Val Ala Ala Phe Phe Ala Phe Arg Tyr Val Leu Gln Leu Gln Arg		
785	790	795
Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu Leu Lys Thr		
805	810	815
Ser Asp Pro Gly Gly Val Gly Gly Glu Glu Gly Ala Glu Gly		
820	825	830
Gly Gly Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg		
835	840	845
Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Arg		
850	855	860
Lys Lys Gly Thr Ser Ala Leu Leu Ser Ser Lys Val Thr Asn Met Val		
865	870	875
880		
Leu Arg Lys Arg Asn Lys Ala Arg Tyr Ser Pro Leu His Asn Glu Asp		
885	890	895
Glu Ala Gly Asp Glu Asp Glu Leu		
900		

<210> 35
 <211> 394
 <212> PRT
 <213> human herpesvirus 1

<400> 35		
Met Gly Gly Ala Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val		
1	5	10
15		
Ile Val Gly Leu His Gly Val Arg Ser Lys Tyr Ala Leu Val Asp Ala		
20	25	30
Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro		
35	40	45
Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Arg Arg Val Tyr His		
50	55	60

Ile Gln Ala Gly Leu Pro Asp Pro Phe Gln Pro Pro Ser Leu Pro Ile
 65 70 75 80
 Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu
 85 90 95
 Asn Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Glu Asp
 100 105 110
 Val Arg Lys Gln Pro Tyr Asn Leu Thr Ile Ala Trp Phe Arg Met Gly
 115 120 125
 Gly Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Ser
 130 135 140
 Tyr Asn Lys Ser Leu Gly Ala Cys Pro Ile Arg Thr Gln Pro Arg Trp
 145 150 155 160
 Asn Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe
 165 170 175
 Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu
 180 185 190
 Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His
 195 200 205
 Arg Ala Lys Gly Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro
 210 215 220
 Ser Ala Cys Leu Ser Pro Gln Ala Tyr Gln Gln Gly Val Thr Val Asp
 225 230 235 240
 Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val
 245 250 255
 Ala Val Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Ala Pro
 260 265 270
 Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro Asn Ala
 275 280 285
 Thr Gln Pro Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu
 290 295 300
 Glu Asp Pro Val Gly Thr Val Ala Pro Gln Ile Pro Pro Asn Trp His
 305 310 315 320
 Ile Pro Ser Ile Gln Asp Ala Ala Thr Pro Tyr His Pro Pro Ala Thr
 325 330 335
 Pro Asn Asn Met Gly Leu Ile Ala Gly Ala Val Gly Ser Leu Leu
 340 345 350
 Ala Ala Leu Val Ile Cys Gly Ile Val Tyr Trp Met Arg Arg His Thr
 355 360 365
 Gln Lys Ala Pro Lys Arg Ile Arg Leu Pro His Ile Arg Glu Asp Asp
 370 375 380
 Gln Pro Ser Ser His Gln Pro Leu Phe Tyr
 385 390

<210> 36
<211> 393
<212> PRT
<213> human herpesvirus 2

<400> 36
Met Gly Arg Leu Thr Ser Gly Val Gly Thr Ala Ala Leu Leu Val Val
1 5 10 15

Ala Val Gly Leu Arg Val Val Cys Ala Lys Tyr Ala Leu Ala Asp Pro
20 25 30

Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asn Leu Pro
35 40 45

Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Lys Arg Val Tyr His
50 55 60

Ile Gln Pro Ser Leu Glu Asp Pro Phe Gln Pro Pro Ser Ile Pro Ile
65 70 75 80

Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu
85 90 95

His Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Asp Glu
100 105 110

Ala Arg Lys His Thr Tyr Asn Leu Thr Ile Ala Trp Tyr Arg Met Gly
115 120 125

Asp Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Pro
130 135 140

Tyr Asn Lys Ser Leu Gly Val Cys Pro Ile Arg Thr Gln Pro Arg Trp
145 150 155 160

Ser Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe
165 170 175

Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu
180 185 190

Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His
195 200 205

Arg Ala Arg Ala Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro
210 215 220

Ala Ala Cys Leu Thr Ser Lys Ala Tyr Gln Gln Gly Val Thr Val Asp
225 230 235 240

Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val
245 250 255

Ala Leu Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Pro Pro
260 265 270

Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Asp Thr Thr Asn Ala
275 280 285

Thr Gln Pro Glu Leu Val Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu
290 295 300

Glu Asp Pro Ala Gly Thr Val Ser Ser Gln Ile Pro Pro Asn Trp His
305 310 315 320

Ile Pro Ser Ile Gln Asp Val Ala Pro His His Ala Pro Ala Ala Pro
325 330 335

Ser Asn Pro Gly Leu Ile Ile Gly Ala Leu Ala Gly Ser Thr Leu Ala
340 345 350

Val Leu Val Ile Gly Gly Ile Ala Phe Trp Val Arg Arg Arg Ala Gln
355 360 365

Met Ala Pro Lys Arg Leu Arg Leu Pro His Ile Arg Asp Asp Asp Ala
370 375 380

Pro Pro Ser His Gln Pro Leu Phe Tyr
385 390